

## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/028,309  
Source: DIPÉ  
Date Processed by STIC: 11/26/02

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
Or  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

## Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10 028,309
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 ___ Wrapped Nucleics ___ Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 ___ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 ___ Misaligned Amino ___ Numbering	The numbering under each 5 <sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 ___ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 ___ Variable Length	Sequence(s) ___ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 ___ PatentIn 2.0 ___ "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 ___ Skipped Sequences ___ (OLD RULES)	Sequence(s) ___ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped  Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 ___ Skipped Sequences ___ (NEW RULES)	Sequence(s) ___ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 ✓ ___ Use of n's or Xaa's ___ (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.	
10 ___ Invalid <213> ___ Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 ✓ ___ Use of <220>	Sequence(s) <u>All</u> missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 ___ PatentIn 2.0 ___ "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 ___ Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	



Does Not Comply  
Corrected Diskette Needed

OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/028,309

DATE: 11/26/2002

TIME: 09:41:18

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF4\11262002\J028309.raw

```

3 <110> APPLICANT: CHENNA, Ahmed
4     SINGH, Sharat
5     XIAO, Vivian
W--> 6 <120> TITLE OF INVENTION: Detection of nucleic acid sequences by cleavage and
separation of tag-
W--> 7     containing structures
W--> 8 <130> FILE REFERENCE: 101.01us
W--> 9 <140> CURRENT APPLICATION NUMBER:
C--> 10 <141> CURRENT FILING DATE: 2002-11-06
11 <150> PRIOR APPLICATION NUMBER: US 60/337,686
12 <151> PRIOR FILING DATE: 2001-11-09
13 <150> PRIOR APPLICATION NUMBER: US 09/602,586
14 <151> PRIOR FILING DATE: 2000-06-21
15 <150> PRIOR APPLICATION NUMBER: US 09/561,579
16 <151> PRIOR FILING DATE: 2000-04-28
W--> 17 <160> NUMBER OF SEQ ID: 5
18 <170> SOFTWARE: Microsoft Word 2000
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 31
22 <212> TYPE: DNA
23 <213> ORGANISM: Artificial Sequence
W--> 24 <220> FEATURE: No special biological significance.
W--> 24 <220> FEATURE: No special biological significance.
W--> 25 <221> NAME/KEY:
26 <222> LOCATION:
27 <223> OTHER INFORMATION:
W--> 28 <400> SEQUENCE: 1
29 ccttccttat cctggatctt ggcaaaatcg a
31 <210> SEQ ID NO: 2
32 <211> LENGTH: 31
33 <212> TYPE: DNA
34 <213> ORGANISM: Artificial Sequence
W--> 35 <220> FEATURE: No special biological significance.
W--> 35 <220> FEATURE: No special biological significance.
W--> 36 <221> NAME/KEY:
37 <222> LOCATION: (1)
38 <223> OTHER INFORMATION: Electrophoretic tag attached at this position.
W--> 39 <221> NAME/KEY:
40 <222> LOCATION: (31)
41 <223> OTHER INFORMATION: Biotin attached at this position.
W--> 42 <400> 2
43 tcgattttct ttacattttc tategtatcc g
45 <210> SEQ ID NO: 3
46 <211> LENGTH: 167

```

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

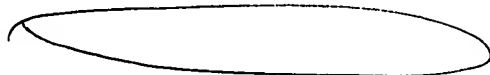
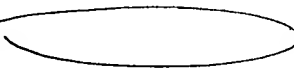

31

Requires explanation of  
genetic source - see  
error summary sheet  
item 11

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/028,309

DATE: 11/26/2002  
TIME: 09:41:18

Input Set : A:\PTO.VSK.txt  
Output Set: N:\CRF4\11262002\J028309.raw

47 <212> TYPE: DNA  
48 <213> ORGANISM: Artificial Sequence  
W--> 49 <220> FEATURE: No special biological significance.  
W--> 49 <220> FEATURE: No special biological significance.  
W--> 50 <221> NAME/KEY:  
51 <222> LOCATION:  
52 <223> OTHER INFORMATION:  - Same error  
W--> 53 <400> SEQUENCE: 3  
54 gtaaaaaccc ttacggggaa gaccatcacc ctcgaggttg aaccctcgga 50  
55 tacgatagaa aatgtaaagg ccaagatcca ggataaggaa ggaattcctc 100  
56 ctgatcagca gagactgatc ttgctggca agcagctgga agatggacgt 150  
57 actttgtctg actacaa 167  
59 <210> SEQ ID NO: 4  
60 <211> LENGTH: 36  
61 <212> TYPE: DNA  
62 <213> ORGANISM: Artificial Sequence  
W--> 63 <220> FEATURE: No special biological significance.  
W--> 63 <220> FEATURE: No special biological significance.  
W--> 64 <221> NAME/KEY:  
65 <222> LOCATION:  
66 <223> OTHER INFORMATION:  - Same error  
W--> 67 <400> SEQUENCE: 4  
68 atcctggatc ttggcaagga ggggaactga tccctc 36  
70 <210> SEQ ID NO: 5  
71 <211> LENGTH: 19  
72 <212> TYPE: DNA  
73 <213> ORGANISM: Artificial Sequence  
W--> 74 <220> FEATURE: No special biological significance.  
W--> 74 <220> FEATURE: No special biological significance.  
W--> 75 <221> NAME/KEY:  
76 <222> LOCATION: (1)  
77 <223> OTHER INFORMATION: Electrophoretic tag attached at this position.  
W--> 78 <221> NAME/KEY:  
79 <222> LOCATION: (2)  
80 <223> OTHER INFORMATION: Abasic site at this position.  
W--> 81 <221>  
82 <222> LOCATION: (19)  
83 <223> OTHER INFORMATION: Biotin attached at this position.  
W--> 84 <400> 5  
W--> 85  attttctat 19

*n detected, must explain  
what residue n represents,  
see error summary  
sheet item 9  
+ p. 3*

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/028,309

DATE: 11/26/2002  
TIME: 09:41:19

Input Set : A:\PTO.VSK.txt  
Output Set: N:\CRF4\11262002\J028309.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa. }

Seq#:5; N Pos. 2

## VERIFICATION SUMMARY

DATE: 11/26/2002

PATENT APPLICATION: US/10/028,309

TIME: 09:41:19

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF4\11262002\J028309.raw

L:6 M:283 W: Missing Blank Line separator, <120> field identifier  
L:8 M:283 W: Missing Blank Line separator, <130> field identifier  
L:9 M:283 W: Missing Blank Line separator, <140> field identifier  
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:17 M:283 W: Missing Blank Line separator, <160> field identifier  
L:24 M:283 W: Missing Blank Line separator, <220> field identifier  
L:24 M:256 W: Invalid Numeric Header Field, <220> has non-blank data  
L:25 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1  
L:28 M:283 W: Missing Blank Line separator, <400> field identifier  
L:28 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:27  
L:35 M:283 W: Missing Blank Line separator, <220> field identifier  
L:35 M:256 W: Invalid Numeric Header Field, <220> has non-blank data  
L:36 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2  
L:39 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2  
L:42 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2  
L:42 M:283 W: Missing Blank Line separator, <400> field identifier  
L:49 M:283 W: Missing Blank Line separator, <220> field identifier  
L:49 M:256 W: Invalid Numeric Header Field, <220> has non-blank data  
L:50 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3  
L:53 M:283 W: Missing Blank Line separator, <400> field identifier  
L:53 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:52  
L:63 M:283 W: Missing Blank Line separator, <220> field identifier  
L:63 M:256 W: Invalid Numeric Header Field, <220> has non-blank data  
L:64 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4  
L:67 M:283 W: Missing Blank Line separator, <400> field identifier  
L:67 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:66  
L:74 M:283 W: Missing Blank Line separator, <220> field identifier  
L:74 M:256 W: Invalid Numeric Header Field, <220> has non-blank data  
L:75 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5  
L:78 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5  
L:81 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5  
L:81 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5  
L:84 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5  
L:84 M:283 W: Missing Blank Line separator, <400> field identifier  
L:85 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0

0